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agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act ggt Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -20 -15 -10
gga cag caa atg ggt cgc gga tcc ctc acc gac gaa cag ata cag Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln -5 1 5
aaa agg aac aag atc agc aaa gaa tgc cag cag gtg tcc gga gtg Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val 10 15 20
tcc caa gag acg atc gac aaa gtc cgc aca ggt gtc ttg gtc gat 276 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp 25 30 35
gat ccc aaa atg aag aag cac gtc ctc tgc ttc tcg aag aaa act 321 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr 40 45 50
gga gtg gca acc gaa gcc gga gac acc aat gtg gag gta ctc aaa 366 Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys 55 60 65
gcc aag ctg aag cat gtg gcc agc gac gaa gaa gtg gac aag atc Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile 70 75 80
gtg cag aag tgc gtg gtc aag aag gcc aca cca gag gaa acg gct 456 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95
tat gac acc ttc aag tgt att tac gac agt aaa cct gat ttc tct 501

Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110

cct att gat taa ctcgagcacc accaccacca ccactgagat 543
Pro Ile Asp ...
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<213> Tenebrio molitor

<223> Mature Protein with His-tag, Clone 2.3

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Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys $1 \hspace{1cm} 5 \hspace{1cm} 10$

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu 65 70 75

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<211> 776

<212> DNA

<213> Tenebrio molitor

<223> His-tagged, Signal plus, Tm 13.17

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		caa Gln						Glu							1	86
		gag Glu													2	31
		ctg Leu													2	76
~ _		ctg Leu		_		-			-			_	_		3	21
_	_	caa Gln													3	166
		cct Pro													4	111
		ctg Leu													4	156
agg Arg	gag Glu	aag Lys	gtg Val 70	agg Arg	aag Lys	gtc Val	act Thr	gac Asp 75	aac Asn	gac Asp	gaa Glu	gaa Glu	act Thr 80	gag Glu	Ę	501
		atc Ile		_	_	_	-	-	-	-					5	546
_		ttc Phe					_	_	Met			_			Ę	591
		cca Pro		-	tga	acc	acca	cga	ctag	taga	tg g	ttca	aatg	g	6	639
tgt	gctt	tac	atat	aaaa	at a	aagt	gttt	c tg	atgt	aaaa	aaa	aaaa	aaa		6	589
aaa	aaaa	aaa a	aact	cgag	ag t	attc	taga	g cg	gccg	cggg	ccc	atcg	ttt		7	739

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96

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	cag Gln															186
	aac Asn 10															231
	gag Glu 25									Asp						276
	aaa Lys 40	_		_		_		_								321
	gcc Ala 55									Asp				_		366
	gtg Val 70															411
	aat Asn 85															456
	aat Asn 100				_	_	_			-		-				501
	gtt Val 115	_	tga	ctc	gagc	acc ·	acca	ccac	ca c	cact	gaga	t				543
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Arg	Gly	Ser -15		Met	Ala	Ser	Met -10		Gly	Gly	Gln	Gln -5	Met	Gly	Arg	

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys	
1 5 10 15	:
Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg 20 25 30	ſ
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys 35 40 45	S
Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val 50 55 60	-
Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu 65 70 75	1
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aaggagatat acc atg ggc agc agc cat cat cat cat cac agc Met Gly Ser Ser His His His His His Ser -55 agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act ggt Ser Gly Leu Val Pro Arg Gly Ser His Met-Ala Ser Met Thr Gly	96
aaggagatat acc atg ggc agc agc cat cat cat cat cac agc Met Gly Ser Ser His His His His His Ser -55 agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act ggt Ser Gly Leu Val Pro Arg Gly Ser His Met-Ala Ser Met Thr Gly -45 -40 -35 gga cag caa atg ggt cgc gga tcc gaa ttc gca cga gca aaa atg Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	96
aaggagatat acc atg ggc agc agc cat cat cat cat cac agc Met Gly Ser Ser His His His His His Ser -55 -50 agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act ggt Ser Gly Leu Val Pro Arg Gly Ser His Met-Ala Ser Met Thr Gly -45 -40 -35 gga cag caa atg ggt cgc gga tcc gaa ttc gca cga gca aaa atg Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 aaa ctc ctc ttg tgc ttt gct ttc gcc gcc atc gtc atc gga gct Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	96 141 186
aaggagatat acc atg ggc agc agc cat cat cat cat cac agc Met Gly Ser Ser His His His His His Ser -55 -50 agc ggc ctg gtg ccg cgc ggc agc cat atg gct agc atg act ggt Ser Gly Leu Val Pro Arg Gly Ser His Met-Ala Ser Met Thr Gly -45 -40 gga cag caa atg ggt cgc gga tcc gaa ttc gca cga gca aaa atg Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 aaa ctc ctc ttg tgc ttt gct ttc gcc gcc atc gtc atc gga gct Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5 cag gct ctc acc gac gaa cag ata cag aaa agg aac aag atc agc Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	96 141 186 231

20 25 aaa gtc cgc aca ggt gtc ttg gtc gac gat ccc aaa atg aag aag 366 Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 35 411 cac gtc ctc tgc ttc tcg aag aaa act gga gtg gca acc gaa gcc His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 gga gac acc aat gtg gag gta ctc aaa gcc aag ctg aag cat gtg 456 Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 gcc agc gac gaa gag gtg gac aag atc gtg cag aag tgc gtg gtc 501 Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 aag aag gcc aca cca gag gaa acg gct tat gac acc ttc aag gtt 546 Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val 90 95 595 att tac gac agt aaa cct gat ttc tct cct att gat taa ttgttttgta Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp 110 645 681 aaaaaactcg agcaccacca ccaccaccac tgagat <210> 29 <211> 173 <212> PRT <213> Tenebrio molitor <223> Precursor protein with His-tag, Clone 3.4 <400> 29 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro -50 -55 Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg -35 Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala -25 -20 Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp

Pro		Met	Lys	Lys	His		Leu	Cys	Phe	Ser		Lys	Thr	Gly	Val		
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Ala 55	Thr	Glu	Ala	Gly	Asp 60	Thr	Asn	Val	Glu	Val 65	Leu	Lys	Ala	Lys	Leu 70		
Lys	His	Val	Ala	Ser 75	Asp	Glu	Glu	Val	Asp 80	Lys	Ile	Val	Gln	Lys 85	Cys		
Val	Val	Lys	Lys 90	Ala	Thr	Pro	Glu	Glu 95	Thr	Ala	Tyr	Asp	Thr 100	Phe	Lys	,	
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aag	gaga	tat a		atg (Met (Ser E					His :				96	
agc	ggc	tat a ctg Leu	I gtg	Met (ccg	Gly S	Ser S	Ser I	His 1 -30 cat	His I	His 1	His :	His :	His and the His and the His arctical His arc	Ser ggt		96 141	
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agc Ser gga Gly aaa Lys	ggc Gly cag Gln agg Arg	ctg Leu caa Gln aac Asn	gtg Val -20 atg Met -5 aag Lys	ccg Pro ggt Gly atc Ile	cgc Arg cgc Arg agc Ser	ggc Gly gga Gly aaa Lys	agc Ser tcc Ser gaa Glu 15	His 1 -30 cat His -15 ctc Leu 1 tgc Cys	atg Met acc Thr cag Gln	gct Ala gac Asp cag Gln	agc Ser gaa Glu gtg Val	atg Met cag Gln 5 tcc Ser 20	His : -25 act Thr -10 ata Ile gga Gly	ggt Gly cag Gln gtg Val		141 186	
agc Ser gga Gly aaa Lys tcc Ser	ggc Gly cag Gln agg Arg caa Gln	ctg Leu caa Gln aac Asn 10 gag Glu	gtg Val -20 atg Met -5 aag Lys acg Thr	ccg Pro ggt Gly atc Ile atc	cgc Arg cgc Arg agc Ser gac Asp	ggc Gly gga Gly aaa Lys aaa Lys	agc Ser I agc Ser tcc Ser gaa Glu 15 gtc Val 30	cat His -30 cat His -15 ctc Leu 1 tgc Cys cgc Arg	atg Met acc Thr cag Gln aca Thr	gct Ala gac Asp cag Gln ggt Gly	agc Ser gaa Glu gtg Val gtc Val	atg Met cag Gln 5 tcc Ser 20 ttg Leu 35	His : -25 act Thr -10 ata Ile gga Gly gtc Val	ggt Gly cag Gln gtg Val gac Asp		141 186 231	
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Phe -10	Ala	Ala	Ile	Val	Ile -5	Gly	Ala	Gln	Ala	Leu 1	Thr	Asp	Glu	Gln 5	Ile	
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Pro	Lys 40	Met	Lys	Lys	His	Val 45	Leu	Cys	Phe	Ser	Lys 50	Arg	Thr	Gly	Val	
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tcc caa gag acg atc gac aaa gtc cgc aca ggt gtc ttg gtc gac Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp 25 30 35	276
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gcc aag ctg aag cat gtg gcc agc gac gaa gtg gac aag atc Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile 70 75 . 80	411
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1.0

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-	Leu Val Asp Asp Pro Lys 35 40	s Met Lys Lys His Val Leu 45
Cys Phe Ser Lys 5	Arg Thr Gly Val Ala Thi 55	Glu Ala Gly Asp Thr Asn 60
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Val Asp Lys Ile '	Val Gln Lys Cys Val Val 85	l Lys Lys Ala Thr Pro Glu 90
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aaggagatat acc a M agc ggc ctg gtg Ser Gly Leu Val -45 gga cag caa atg	tg ggc agc agc cat cat et Gly Ser Ser His His -55 ccg cgc ggc agc cat ato Pro Arg Gly Ser His Me	cat cat cat cac agc 96 His His His His Ser -50 g gct agc atg act ggt 141 t. Ala Ser Met Thr Gly -35 c gca cga gca aaa atg 186
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aaa gtc cgc aca ggt gtc ttg gtc gac gat ccc aaa atg aag aag Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
cac gtc ctc tgc ttc tcg aag aaa act gga gtg gca acc gaa gcc His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
gga gac acc aat gtg gag gta ctc aaa gcc aag ctg aag cat gtg Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
gcc agc gac gaa gag gtg gac aag atc gtg cag aag tgc gtg gtc Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
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att tac gac agt aaa cct gat ttc tct cct att gat taa ttgttttgta Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp 105 110 115	595
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25

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<211> 25
<212> DNA
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<212> DNA
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<210> 43
<211> 25
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defined as any amino acid.
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					aaa Lys										136
		_		_	aaa Lys		_			_	-	-		-	181
					cac His										226
	_		_	-	gga Gly	~			~ ~	~ ~	-			_	271
					gcc Ala										316
_	_	-		-	aag Lys	_	-				-	-	-		361
_					att Ile		_	-			-				406
	gat Asp 115	taa	ttg	tttt	gta 1	tttg	rctga	aa t	tttga	, acaat	t aaa	aggta	anta		455
tcgt	tat	gna a	aaaa	aaaa	aa aa	aaaa	a								481
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					Seq y am:				Tm :	13.1	7, 'ı	n' d	efin	ed as any	nucleotide,
<400		45 ann <i>i</i>	aar a	ata :	aar 1	vtn v	ctc :	tnn '	tav 1	vtn :	rvn ·	tvo :	nvc ·	rin.	16

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-15 -10

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nng aac aag atc agc aaa rar tgy car nan gnr nny gga gtg tcn Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser 10 15 20	136
caa gag ayn atn rnc aaa gyy cgc ann ggt gnc tng gnn gay gat Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35	181
ccy aaa ntg aar nrn can gty yty tgc ntn ncn arg arn rcy ggn Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50	226
ntg gcn acn gaa ncn gga gan ryn rnn gtn gan gtr ytn arr gnn Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60 65	271
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rtn nan aag tgc gyn gtc aag arr gny acn nyn gar gar acg gyn Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala 85 90 95	361
tny ray acy ttc aar nnt rty nnn ran ary aar ccn ran ttc tcn Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110	406
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-15

-10



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nng nnc nar ayc agc rna rar tgy nar nnn gnr nny gga gtg tcn Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser 10 15 20	136
naa gan ryn atn rnn ara gyy cgc ann ggt gnc tng gnn gay gay Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp 25 30 35	181
ccy aaa ntg aar nnn can nty yty tgc ntn nyn arg rnn nyy grn Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly 40 45 50	226
ntr gyn rcn gaa ncn gga gan ryn rnn gyn gan ryr ytn arr gnn Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala 55 60 65	271
aag ntg ang nrn nnn nnn rnn ann rnn rar rar ryn rrn arr ntn Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile 70 75 80	316
nyn nrn arn nnn nnn nnn nng arn rnn nyn nnn rar rnr nnn nnn Val Gln Lys Cys Val Val Lys Lys Ala Thr'Pro Glu Glu Thr Ala 85 90 95	361
tnn ran nyn yyn aan nnn nny nnn rrn ann arn ccn rnn tyy tyn Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser 100 105 110	406
cnn ryt rnt trn nynnnnnnnn ynngnnnrnr nttyranaat aaagnnnytn Pro Ile Asp 115	458
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ntn ntn ryc nnr ryy yan gcy ntn acy nan rna nnn nnn nag nnr	91

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Ile	Val	Ile -5	Gly	Ala	Gln	Ala	Leu 1	Thr	Asp	Glu	Gln 5	Ile	Gln	Lys	
_	_			-	rnn Lys						_	- 1			136
	_	_			arr Lys		_		-	-					181
					can His										226
	_		_		ggn Gly	_	_		_	_					271
		_			nnn Ala						-				316
_					nnn Val	_			-						361
		_			nnn Cys	_					_				406
	nyn Ile 115		trn	nnn	กทกกเ	nnn g	ynnrı	າກກນ	nn ni	nnnı	nnaa	t aa	annni	nnnn	458
nnnı	nnn	nna a	aaaa	aaaa	aa aa	aaaa	a								484
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	1> : 2> 3> :		ral (Cons	ensu: efin							AFP-	3, 'i	n' defined	as any
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Xaa	Ala	Xaa 1	Thr	Xaa	Xaa	Xaa 5	Xaa	Glx	Xaa	Xaa	Xaa 10	Xaa	Xaa	Ser Xaa	

 Xaa
 Cys
 Xaa
 Xaa
 Xaa
 Ser
 Gly
 Xaa
 Ser
 Glx
 Xaa
 Xaa
 Xaa
 Xaa
 Xaa
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 Xaa
 Xaa
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 Asa
 A